

AMENDMENTS TO THE CLAIMS

1. (cancelled)
2. (original): A sequence determination oligonucleotide suitable for detecting a polymorphic site in a 5' flanking region of a *CYP2C19* gene, said oligonucleotide comprising a sequence selected from the group consisting of SEQ ID NO:2; SEQ ID NO:3; SEQ ID NO:4; SEQ ID NO:5; SEQ ID NO:6; SEQ ID NO:7; SEQ ID NO:20; SEQ ID NO:21, SEQ ID NO:22; SEQ ID NO:23; SEQ ID NO:24; SEQ ID NO:25; SEQ ID NO:26; SEQ ID NO:27; SEQ ID NO:28; SEQ ID NO:29; SEQ ID NO:30; SEQ ID NO:31; SEQ ID NO:32; SEQ ID NO:33, SEQ ID NO:34; SEQ ID NO:35; SEQ ID NO:36; and SEQ ID NO:37.
3. (original): An oligonucleotide primer pair suitable for amplifying a 5' flanking region of a *CYP2C19* gene, said primer pair having sequences selected from the group consisting of: SEQ ID NO:8 and SEQ ID NO:9; SEQ ID NO:10 and SEQ ID NO:11; SEQ ID NO:12 and SEQ ID NO:13; SEQ ID NO:14 and SEQ ID NO:15; SEQ ID NO:16 and SEQ ID NO:17; and SEQ ID NO:18 and SEQ ID NO:19.
4. (original): An isolated polynucleotide comprising a sequence as set forth in SEQ ID NO: 1.
5. (original): A kit comprising:
 - a) a first pair of oligonucleotide primers for amplifying the polymorphic region corresponding to position 352 of SEQ ID NO:1;
 - b) a second primer pair for amplifying the polymorphic region corresponding to position 1060 of SEQ ID NO: 1;
 - c) a first sequence determination oligonucleotide comprising a sequence selected from the group consisting of SEQ ID NO:3; SEQ ID NO:6; SEQ ID NO:22; SEQ ID NO:23; SEQ ID NO:27; SEQ ID NO:30; SEQ ID NO:33; and SEQ ID NO:36; and

d) a second sequence determination oligonucleotide comprising a sequence selected from the group consisting of SEQ ID NO:4; SEQ ID NO:7; SEQ ID NO:24; SEQ ID NO:25; SEQ ID NO:28; SEQ ID NO:31; SEQ ID NO:34; and SEQ ID NO:37.

6. (original): The kit of claim 5, wherein the first primer pair selected from the group consisting of SEQ ID NO:8 and SEQ ID NO:9; SEQ ID NO:16 and SEQ ID NO:17; and SEQ ID NO:18 and SEQ ID NO:19; and the second primer pair is selected from the group consisting of SEQ ID NO: 10 and SEQ ID NO: 11; SEQ ID NO:12 and SEQ ID NO:13; and SEQ ID NO:14 and SEQ ID NO:15.

7. (new): A method for determining a human's capacity to metabolize a substrate of a CYP2C19 enzyme, which comprises:

identifying nucleotides at three or more polymorphic sites in a CYP2C19 flanking region in a strand of a human nucleic acid, and

predicting the capacity from the nucleotides identified at the two or more polymorphic sites.

8. (new): The method of claim 7, which comprises isolating the nucleic acid from the human.

9. (new): The method of claim 8, wherein the nucleic acid is DNA..

10. (new): The method of 9, wherein the DNA is single-stranded.

11. (new): The method of claim 7, wherein the polymorphic sites are at positions 352 and 1060 of SEQ ID NO: 1.